#5

SEQUENCE LISTING

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LESAGE, FLORIAN
ROMEY, GEORGES

<120> HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND RILUZOLE

<130> 1256-R-00

<140> 09/892,360
<141> 2001-06-27

<150> 60/214,559
<151> 2000-06-27

<160> 25

<170> PatentIn Ver. 2.1

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<212> DNA
<213> Homo sapiens

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<222> (1)..(1614)
<223> ORF of human TREK2 cDNA

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Met Phe Phe Leu Tyr Thr Asp Phe Phe Leu Ser Leu Val Ala Val Pro
  1               5                  10                  15

gca gca gca ccg gtg tgc cag ccc aag agc gcc act aac ggg caa ccc   96
Ala Ala Ala Pro Val Cys Gln Pro Lys Ser Ala Thr Asn Gly Gln Pro
             20                  25                  30

ccg gct ccg gct ccg act cca act ccg cgc ctg tcc att tcc tcc cga   144
Pro Ala Pro Ala Pro Thr Pro Thr Pro Arg Leu Ser Ile Ser Ser Arg
         35                  40                  45

gcc aca gtg gta gcc agg atg gaa ggc acc tcc caa ggg ggc ttg cag   192
Ala Thr Val Val Ala Arg Met Glu Gly Thr Ser Gln Gly Gly Leu Gln
     50                  55                  60

acc gtc atg aag tgg aag acg gtg gtt gcc atc ttt gtg gtt gtg gtg   240
Thr Val Met Lys Trp Lys Thr Val Val Ala Ile Phe Val Val Val Val
 65                  70                  75                  80

gtc tac ctt gtc act ggc ggt ctt gtc ttc cgg gca ttg gag cag ccc   288
Val Tyr Leu Val Thr Gly Gly Leu Val Phe Arg Ala Leu Glu Gln Pro
                85                  90                  95
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ttt gag agc agc cag aag aat acc atc gcc ttg gag aag gcg gaa ttc   336
Phe Glu Ser Ser Gln Lys Asn Thr Ile Ala Leu Glu Lys Ala Glu Phe
            100                 105                 110

ctg cgg gat cat gtc tgt gtg agc ccc cag gag ctg gag acg ttg atc   384
Leu Arg Asp His Val Cys Val Ser Pro Gln Glu Leu Glu Thr Leu Ile
        115                 120                 125

cag cat gct ctt gat gct gac aat gcg gga gtc agt cca ata gga aac   432
Gln His Ala Leu Asp Ala Asp Asn Ala Gly Val Ser Pro Ile Gly Asn
    130                 135                 140

tct tcc aac aac agc agc cac tgg gac ctc ggc agt gcc ttt ttc ttt   480
Ser Ser Asn Asn Ser Ser His Trp Asp Leu Gly Ser Ala Phe Phe Phe
145                 150                 155                 160

gct gga act gtc att acg acc ata ggg tat ggg aat att gct ccg agc   528
Ala Gly Thr Val Ile Thr Thr Ile Gly Tyr Gly Asn Ile Ala Pro Ser
                165                 170                 175

act gaa gga ggc aaa atc ttt tgt att tta tat gcc atc ttt gga att   576
Thr Glu Gly Gly Lys Ile Phe Cys Ile Leu Tyr Ala Ile Phe Gly Ile
            180                 185                 190

cca ctc ttt ggt ttc tta ttg gct gga att gga gac caa ctt gga acc   624
Pro Leu Phe Gly Phe Leu Leu Ala Gly Ile Gly Asp Gln Leu Gly Thr
        195                 200                 205

atc ttt ggg aaa agc att gca aga gtg gag aag gtc ttt cga aaa aag   672
Ile Phe Gly Lys Ser Ile Ala Arg Val Glu Lys Val Phe Arg Lys Lys
    210                 215                 220

caa gtg agt cag acc aag atc cgg gtc atc tca acc atc ctg ttc atc   720
Gln Val Ser Gln Thr Lys Ile Arg Val Ile Ser Thr Ile Leu Phe Ile
225                 230                 235                 240

ttg gcc ggc tgc att gtg ttt gtg acg atc cct gct gtc atc ttt aag   768
Leu Ala Gly Cys Ile Val Phe Val Thr Ile Pro Ala Val Ile Phe Lys
                245                 250                 255

tac atc gag ggc tgg acg gcc ttg gag tcc att tac ttt gtg gtg gtc   816
Tyr Ile Glu Gly Trp Thr Ala Leu Glu Ser Ile Tyr Phe Val Val Val
            260                 265                 270

act ctg acc acg gtg ggc ttt ggt gat ttt gtg gca ggg gga aac gct   864
Thr Leu Thr Thr Val Gly Phe Gly Asp Phe Val Ala Gly Gly Asn Ala
        275                 280                 285

ggc atc aat tat cgg gag tgg tat aag ccc cta gtg tgg ttt tgg atc   912
Gly Ile Asn Tyr Arg Glu Trp Tyr Lys Pro Leu Val Trp Phe Trp Ile
    290                 295                 300

ctt gtt ggc ctt gcc tac ttt gca gct gtc ctc agt atg atc gga gat   960
Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu Ser Met Ile Gly Asp
305                 310                 315                 320
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tgg cta cgg gtt ctg tcc aaa aag aca aaa gaa gag gtg ggt gaa atc   1008
Trp Leu Arg Val Leu Ser Lys Lys Thr Lys Glu Glu Val Gly Glu Ile
                325                 330                 335

aag gcc cat gcg gca gag tgg aag gcc aat gtc acg gct gag ttc cgg   1056
Lys Ala His Ala Ala Glu Trp Lys Ala Asn Val Thr Ala Glu Phe Arg
            340                 345                 350

gag aca cgg cga agg ctc agc gtg gag atc cac gat aag ctg cag cgg   1104
Glu Thr Arg Arg Arg Leu Ser Val Glu Ile His Asp Lys Leu Gln Arg
        355                 360                 365

gcg gcc acc atc cgc agc atg gag cgc cgg cgg ctg ggc ctg gac cag   1152
Ala Ala Thr Ile Arg Ser Met Glu Arg Arg Arg Leu Gly Leu Asp Gln
    370                 375                 380

cgg gcc cac tca ctg gac atg ctg tcc ccc gag aag cgc tct gtc ttt   1200
Arg Ala His Ser Leu Asp Met Leu Ser Pro Glu Lys Arg Ser Val Phe
385                 390                 395                 400

gct gcc ctg gac acc ggc cgc ttc aag gcc tca tcc cag gag agc atc   1248
Ala Ala Leu Asp Thr Gly Arg Phe Lys Ala Ser Ser Gln Glu Ser Ile
                405                 410                 415

aac aac cgg ccc aac aac ctg cgc ctg aag ggg ccg gag cag ctg aac   1296
Asn Asn Arg Pro Asn Asn Leu Arg Leu Lys Gly Pro Glu Gln Leu Asn
            420                 425                 430

aag cat ggg cag ggt gcg tcc gag gac aac atc atc aac aag ttc ggg   1344
Lys His Gly Gln Gly Ala Ser Glu Asp Asn Ile Ile Asn Lys Phe Gly
        435                 440                 445

tcc acc tcc aga ctc acc aag agg aaa aac aag gac ctc aaa aag acc   1392
Ser Thr Ser Arg Leu Thr Lys Arg Lys Asn Lys Asp Leu Lys Lys Thr
    450                 455                 460

ttg ccc gag gac gtt cag aaa atc tac aag acc ttc cgg aat tac tcc   1440
Leu Pro Glu Asp Val Gln Lys Ile Tyr Lys Thr Phe Arg Asn Tyr Ser
465                 470                 475                 480

ctg gac gag gag aag aaa gag gag gag acg gaa aag atg tgt aac tca   1488
Leu Asp Glu Glu Lys Lys Glu Glu Glu Thr Glu Lys Met Cys Asn Ser
                485                 490                 495

gac aac tcc agc aca gcc atg ctg acg gac tgt atc cag cag cac gct   1536
Asp Asn Ser Ser Thr Ala Met Leu Thr Asp Cys Ile Gln Gln His Ala
            500                 505                 510

gag ttg gag aac gga atg ata ccc acg gac acc aaa gac cgg gag ccg   1584
Glu Leu Glu Asn Gly Met Ile Pro Thr Asp Thr Lys Asp Arg Glu Pro
        515                 520                 525

gag aac aac tca tta ctt gaa gac aga aac                           1614
Glu Asn Asn Ser Leu Leu Glu Asp Arg Asn
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<212> PRT
<213> Homo sapiens

<400> 2

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Met Phe Phe Leu Tyr Thr Asp Phe Phe Leu Ser Leu Val Ala Val Pro
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Ala Ala Ala Pro Val Cys Gln Pro Lys Ser Ala Thr Asn Gly Gln Pro
             20                  25                  30

Pro Ala Pro Ala Pro Thr Pro Thr Pro Arg Leu Ser Ile Ser Ser Arg
         35                  40                  45

Ala Thr Val Val Ala Arg Met Glu Gly Thr Ser Gln Gly Gly Leu Gln
     50                  55                  60

Thr Val Met Lys Trp Lys Thr Val Val Ala Ile Phe Val Val Val Val
 65                  70                  75                  80

Val Tyr Leu Val Thr Gly Gly Leu Val Phe Arg Ala Leu Glu Gln Pro
                 85                  90                  95

Phe Glu Ser Ser Gln Lys Asn Thr Ile Ala Leu Glu Lys Ala Glu Phe
            100                 105                 110

Leu Arg Asp His Val Cys Val Ser Pro Gln Glu Leu Glu Thr Leu Ile
        115                 120                 125

Gln His Ala Leu Asp Ala Asp Asn Ala Gly Val Ser Pro Ile Gly Asn
    130                 135                 140

Ser Ser Asn Asn Ser Ser His Trp Asp Leu Gly Ser Ala Phe Phe Phe
145                 150                 155                 160

Ala Gly Thr Val Ile Thr Thr Ile Gly Tyr Gly Asn Ile Ala Pro Ser
                165                 170                 175

Thr Glu Gly Gly Lys Ile Phe Cys Ile Leu Tyr Ala Ile Phe Gly Ile
            180                 185                 190

Pro Leu Phe Gly Phe Leu Leu Ala Gly Ile Gly Asp Gln Leu Gly Thr
        195                 200                 205

Ile Phe Gly Lys Ser Ile Ala Arg Val Glu Lys Val Phe Arg Lys Lys
    210                 215                 220

Gln Val Ser Gln Thr Lys Ile Arg Val Ile Ser Thr Ile Leu Phe Ile
225                 230                 235                 240

Leu Ala Gly Cys Ile Val Phe Val Thr Ile Pro Ala Val Ile Phe Lys
                245                 250                 255

Tyr Ile Glu Gly Trp Thr Ala Leu Glu Ser Ile Tyr Phe Val Val Val
            260                 265                 270
```

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Thr Leu Thr Thr Val Gly Phe Gly Asp Phe Val Ala Gly Gly Asn Ala
        275                 280                 285

Gly Ile Asn Tyr Arg Glu Trp Tyr Lys Pro Leu Val Trp Phe Trp Ile
    290                 295                 300

Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu Ser Met Ile Gly Asp
305                 310                 315                 320

Trp Leu Arg Val Leu Ser Lys Lys Thr Lys Glu Glu Val Gly Glu Ile
                325                 330                 335

Lys Ala His Ala Ala Glu Trp Lys Ala Asn Val Thr Ala Glu Phe Arg
            340                 345                 350

Glu Thr Arg Arg Arg Leu Ser Val Glu Ile His Asp Lys Leu Gln Arg
        355                 360                 365

Ala Ala Thr Ile Arg Ser Met Glu Arg Arg Arg Leu Gly Leu Asp Gln
    370                 375                 380

Arg Ala His Ser Leu Asp Met Leu Ser Pro Glu Lys Arg Ser Val Phe
385                 390                 395                 400

Ala Ala Leu Asp Thr Gly Arg Phe Lys Ala Ser Ser Gln Glu Ser Ile
                405                 410                 415

Asn Asn Arg Pro Asn Asn Leu Arg Leu Lys Gly Pro Glu Gln Leu Asn
            420                 425                 430

Lys His Gly Gln Gly Ala Ser Glu Asp Asn Ile Ile Asn Lys Phe Gly
        435                 440                 445

Ser Thr Ser Arg Leu Thr Lys Arg Lys Asn Lys Asp Leu Lys Lys Thr
    450                 455                 460

Leu Pro Glu Asp Val Gln Lys Ile Tyr Lys Thr Phe Arg Asn Tyr Ser
465                 470                 475                 480

Leu Asp Glu Glu Lys Lys Glu Glu Glu Thr Glu Lys Met Cys Asn Ser
                485                 490                 495

Asp Asn Ser Ser Thr Ala Met Leu Thr Asp Cys Ile Gln Gln His Ala
            500                 505                 510

Glu Leu Glu Asn Gly Met Ile Pro Thr Asp Thr Lys Asp Arg Glu Pro
        515                 520                 525

Glu Asn Asn Ser Leu Leu Glu Asp Arg Asn
    530                 535
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 4
tctggctgct ctcaaagggc tgct 24

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
gacgatccct gctgtcatct t 21

<210> 6
<211> 23
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<220>
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ttgcagctgt cctcagtaga tcg 23

<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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tagaatcgag gtcgacggta tc 22

<210> 8
<211> 25

<212> DNA
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<220>
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<210> 9
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<220>
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<210> 10
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<210> 11
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<220>
<223> Description of Artificial Sequence: Primer

<400> 11
gaggcccggc caggggatcc tg 22

<210> 12
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<220>
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<400> 12
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<210> 13
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<220>
<223> Description of Artificial Sequence: Primer

<400> 13
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<210> 14
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<220>
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gatccacctg caacgtagtc 20

<210> 15
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<220>
<223> Description of Artificial Sequence: Primer

<400> 15
actgccgagg tcccagtggc tgctgtt 27

<210> 16
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<212> DNA
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<220>
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<400> 16
tcaggctgcc agctggactg 20

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<210> 18
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<212> PRT
<213> Mus musculus

<400> 18

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  1               5                  10                  15

Lys Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg
             20                  25                  30

Val Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser
         35                  40                  45

Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val
     50                  55                  60

Phe Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile
 65                  70                  75                  80

Val Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser
                 85                  90                  95

Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala
            100                 105                 110

Gly Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp
        115                 120                 125

Leu Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly
    130                 135                 140

Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile
145                 150                 155                 160

Ile Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly
                165                 170                 175

Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val
            180                 185                 190

Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile
        195                 200                 205

Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala
    210                 215                 220

Leu Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp
225                 230                 235                 240

Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp
                245                 250                 255

Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro
            260                 265                 270
```

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Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val
        275                 280                 285

Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys
    290                 295                 300

Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn
305                 310                 315                 320

Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile
                325                 330                 335

Tyr Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala
            340                 345                 350

Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr
        355                 360                 365

Leu Ser Val Asn His Leu Thr Asn Glu Arg Asp Val Leu Pro Pro Leu
    370                 375                 380

Leu Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Thr Pro His Cys Ala
385                 390                 395                 400

Gly Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
                405                 410
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<210> 19
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<212> PRT
<213> Mus musculus

<400> 19

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Leu Val Ser Gly Ala Leu Val Phe Gln Ala Leu Glu Gln Pro His Glu
            20                  25                  30

Gln Gln Ala Gln Lys Lys Met Asp His Gly Arg Asp Gln Phe Leu Arg
        35                  40                  45

Asp His Pro Cys Val Ser Gln Lys Ser Leu Glu Asp Phe Ile Lys Leu
    50                  55                  60

Leu Val Glu Ala Leu Gly Gly Gly Ala Asn Pro Glu Thr Ser Trp Thr
65                  70                  75                  80

Asn Ser Ser Asn His Ser Ser Ala Trp Asn Leu Gly Ser Ala Phe Phe
                85                  90                  95

Phe Ser Gly Thr Ile Ile Thr Thr Ile Gly Tyr Gly Asn Ile Val Leu
            100                 105                 110

His Thr Asp Ala Gly Arg Leu Phe Cys Ile Phe Tyr Ala Leu Val Gly
        115                 120                 125
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Ile Pro Leu Phe Gly Met Leu Leu Ala Gly Val Gly Asp Arg Leu Gly
    130                 135                 140

Ser Ser Leu Arg Arg Gly Ile Gly His Ile Glu Ala Ile Phe Leu Lys
145                 150                 155                 160

Trp His Val Pro Pro Gly Leu Val Arg Ser Leu Ser Ala Val Leu Phe
                165                 170                 175

Leu Leu Ile Gly Cys Leu Leu Phe Val Leu Thr Pro Thr Phe Val Phe
            180                 185                 190

Ser Tyr Met Glu Ser Trp Ser Lys Leu Glu Ala Ile Tyr Phe Val Ile
        195                 200                 205

Val Thr Leu Thr Thr Val Gly Phe Gly Asp Tyr Val Pro Gly Asp Gly
    210                 215                 220

Thr Gly Gln Asn Ser Pro Ala Tyr Gln Pro Leu Val Trp Phe Trp Ile
225                 230                 235                 240

Leu Phe Gly Leu Ala Tyr Phe Ala Ser Val Leu Thr Thr Ile Gly Asn
                245                 250                 255

Trp Leu Arg Ala Val Ser Arg Arg Thr Arg Ala Glu Met Gly Gly Leu
            260                 265                 270

Thr Ala Gln Ala Ala Ser Trp Thr Gly Thr Val Thr Ala Arg Val Thr
        275                 280                 285

Gln Arg Thr Gly Pro Ser Ala Pro Pro Pro Glu Lys Glu Gln Pro Leu
    290                 295                 300

Leu Pro Ser Ser Leu Pro Ala Pro Pro Ala Val Val Glu Pro Ala Gly
305                 310                 315                 320

Arg Pro Gly Ser Pro Ala Pro Ala Glu Lys Val Glu Thr Pro Ser Pro
                325                 330                 335

Pro Thr Ala Ser Ala Leu Asp Tyr Pro Ser Glu Asn Leu Ala Phe Ile
            340                 345                 350

Asp Glu Ser Ser Asp Thr Gln Ser Glu Arg Gly Cys Ala Leu Pro Arg
        355                 360                 365

Ala Pro Arg Gly Arg Arg Arg Pro Asn Pro Ser Lys Lys Pro Ser Arg
    370                 375                 380

Pro Arg Gly Pro Gly Arg Leu Arg Asp Lys Ala Val Pro Val
385                 390                 395
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<210> 20
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ctttgctctt cctag 15

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